



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/762,759

DATE: 08/30/2004

TIME: 14:40:54

Input Set : N:\Crf3\RULE60\10762759.raw.txt

Output Set: N:\CRF4\08302004\J762759.raw

```

1 <110> APPLICANT: Mathur, Brian
2   Turner, C. Alexander Jr.
3   Abuin, Alejandro
4   Friedrich, Glenn
5   Zambrowicz, Brian
6   Sands, Arthur T.
7 <120> TITLE OF INVENTION: Novel Human Kinase Protein and
8   Polynucleotides Encoding the Same
9 <130> FILE REFERENCE: LEX-0083-USA
10 <140> CURRENT APPLICATION NUMBER: US/10/762,759
11 <141> CURRENT FILING DATE: 2004-01-22
12 <150> PRIOR APPLICATION NUMBER: US/09/707,121
13 <151> PRIOR FILING DATE: 2000-11-06
14 <150> PRIOR APPLICATION NUMBER: US 60/164,289
15 <151> PRIOR FILING DATE: 1999-11-08
16 <160> NUMBER OF SEQ ID NOS: 2
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2682
21 <212> TYPE: DNA
22 <213> ORGANISM: homo sapiens
23 <400> SEQUENCE: 1
24   atgtttcccc tgaaggacgc tgaaatggga gcctttacct tctttgcctc ggctctgcc 60
25   catgatgttt ttggaagcaa tggacttctc ctcacaccaa attccatcaa aattttaggg 120
26   cgcttttcaaa tccttaaaac catcacccat ccagactct gccagtatgt ggatatttct 180
27   aggggaaagc atgaacgact agtggtcgtg gctgaacatt gtgaacgtag tctggaagac 240
28   ttgcttcgag aaaggaaacc tgtgagctgt tcaacggttt tgtgtatagc atttgagggt 300
29   cttcagggct tgcagtatat gaacaaacat ggtatagtac acagggcatt gtctctcat 360
30   aatatcctgt tggaccgaaa gggacatatt aaattggcta aatttggact ttatcacatg 420
31   acagctcatg gtgatgatgt tgatttccca atagggatc cctcgtactt ggcccctgag 480
32   gtaattgcac aggggaattt caaaaccact gatcacatgc caagtaaaaa accattgcct 540
33   tctggcccca aatcagatgt atggctctctt ggaatcattt tatttgagct ttgtgtggga 600
34   agaâaattat ttcagagctt ggatatttct gaaagactaa aatttttgct tactttggat 660
35   tgtgtagatg acactttaat agttctggct gaagagcatg gttgtttgga cattataaag 720
36   gagcttctcg aaactgtgat agatcttttg aataagtgcc ttaccttcca tccttctaag 780
37   aggccaaccc cagatgaatt aatgaaggac aaagtattca gtgaggtatc acctttatat 840
38   acccccttta ccaaacctgc cagtctgttt tcattctctc tgagatgtgc tgatttaact 900
39   ctgcctgagg atatcagtc gttgtgtaaa gatataaata atgattacct ggcagaaaga 960
40   tctattgaag aagtgtatta cttttggtgt ttggctggag gtgacttgga gaaagagctt 1020
41   gtcaacaagg aaatcattcg atccaaacca cctatctgca cactcccaa tttctcttt 1080
42   gaggatggtg aaagctttgg acaaggtcga gatagaagct cgctttttaga tgataccact 1140
43   gtgacattgt cgttatgcca gctaagaaat agattgaaag atgttggtgg agaagcattt 1200
44   taccattac ttgaagatga ccagtctaatt ttacctcatt caaacagcaa taatgagttg 1260

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45 tctgcagctg ccacgctccc tttaatcatc agagagaagg atacagagta ccaactaaat 1320
46 agaattattc tcttcgacag gctgctaaag gcttatccat ataaaaaaaa ccaaatctgg 1380
47 aaagaagcaa gagttgacat tcctcctctt atgagagggt taacctgggc tgctcttctg 1440
48 ggagttgagg gagctattca tgccaagtac gatgcaattg ataaagacac tccaattcct 1500
49 acagatagac aaattgaagt ggatattcct cgctgtcatc agtacgatga actgttatca 1560
50 tcaccagaag gtcatgcaaa atttaggcgt gtattaaaag cctgggtagt gtctcatcct 1620
51 gatcttgtgt attggcaagg tcttgactca ctttgtgctc cattcctata tctaaacttc 1680
52 aataatgaag ccttggctta tgcatgtatg tctgctttta ttcccaaata cctgtataac 1740
53 ttcttcttaa aagacaactc acatgtaata caagagtatc tgactgtctt ctctcagatg 1800
54 attgcatttc atgatccaga gctgagtaat catctcaatg agattgggtt cattccagat 1860
55 ctctatgcca tcccttgggt tcttaccatg tttactcatg tatttccact acacaaaatt 1920
56 ttccacctct gggatacctt actacttggg aattcctctt tcccattctg tattggagta 1980
57 gcaattcttc agcagctgcg ggaccggcct ttggctaatt gctttaatga gtgtattcct 2040
58 ctcttctccg atttaccaga aattgacatt gaacgctgtg tgagagaatc tatcaacctg 2100
59 ttttgttggg ctctataaag tgctacttac agacagcatg ctcaacctcc aaagccatct 2160
60 tctgacagca gtggaggcag aagttcggca ccttatttct ctgctgagtg tccagatcct 2220
61 ccaaagacag atctgtcaag agaattccatc ccattaaatg acctgaagtc agaagtatca 2280
62 ccacggattt cagcagagga cctgattgac ttgtgtgagc tcacagtga aggccacttc 2340
63 aaaacaccca gcaagaaaac aaagtccagt aaaccaaagc tcttgggtgt tgacatccgg 2400
64 aatagtgaag actttattcg tggtcacatt tcaggaagca tcaacattcc attcagtgtc 2460
65 gccttctactg cagaagggga gcttaccagc ggcccttaca ctgctatgct ccagaacttc 2520
66 aaaggggaagg tcattgtcat cgtggggcat gtggcaaaac acacagctga gtttgagct 2580
67 caccttgtga agatgaaata tccaagaatc tgtattctag atggtggcat taataaaata 2640
68 aagccaacag gcctcctcac catcccatct cctcaaatat ga 2682

```

70 &lt;210&gt; SEQ ID NO: 2

71 &lt;211&gt; LENGTH: 893

72 &lt;212&gt; TYPE: PRT

73 &lt;213&gt; ORGANISM: homo sapiens

74 &lt;400&gt; SEQUENCE: 2

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75 Met Phe Pro Leu Lys Asp Ala Glu Met Gly Ala Phe Thr Phe Phe Ala
76 1 5 10 15
77 Ser Ala Leu Pro His Asp Val Cys Gly Ser Asn Gly Leu Pro Leu Thr
78 20 25 30
79 Pro Asn Ser Ile Lys Ile Leu Gly Arg Phe Gln Ile Leu Lys Thr Ile
80 35 40 45
81 Thr His Pro Arg Leu Cys Gln Tyr Val Asp Ile Ser Arg Gly Lys His
82 50 55 60
83 Glu Arg Leu Val Val Val Ala Glu His Cys Glu Arg Ser Leu Glu Asp
84 65 70 75 80
85 Leu Leu Arg Glu Arg Lys Pro Val Ser Cys Ser Thr Val Leu Cys Ile
86 85 90 95
87 Ala Phe Glu Val Leu Gln Gly Leu Gln Tyr Met Asn Lys His Gly Ile
88 100 105 110
89 Val His Arg Ala Leu Ser Pro His Asn Ile Leu Leu Asp Arg Lys Gly
90 115 120 125
91 His Ile Lys Leu Ala Lys Phe Gly Leu Tyr His Met Thr Ala His Gly
92 130 135 140
93 Asp Asp Val Asp Phe Pro Ile Gly Tyr Pro Ser Tyr Leu Ala Pro Glu
94 145 150 155 160

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```

95  Val Ile Ala Gln Gly Ile Phe Lys Thr Thr Asp His Met Pro Ser Lys
96                      165                      170                      175
97  Lys Pro Leu Pro Ser Gly Pro Lys Ser Asp Val Trp Ser Leu Gly Ile
98                      180                      185                      190
99  Ile Leu Phe Glu Leu Cys Val Gly Arg Lys Leu Phe Gln Ser Leu Asp
100                     195                      200                      205
101  Ile Ser Glu Arg Leu Lys Phe Leu Leu Thr Leu Asp Cys Val Asp Asp
102                     210                      215                      220
103  Thr Leu Ile Val Leu Ala Glu Glu His Gly Cys Leu Asp Ile Ile Lys
104                     225                      230                      235                      240
105  Glu Leu Pro Glu Thr Val Ile Asp Leu Leu Asn Lys Cys Leu Thr Phe
106                      245                      250                      255
107  His Pro Ser Lys Arg Pro Thr Pro Asp Glu Leu Met Lys Asp Lys Val
108                      260                      265                      270
109  Phe Ser Glu Val Ser Pro Leu Tyr Thr Pro Phe Thr Lys Pro Ala Ser
110                      275                      280                      285
111  Leu Phe Ser Ser Ser Leu Arg Cys Ala Asp Leu Thr Leu Pro Glu Asp
112                     290                      295                      300
113  Ile Ser Gln Leu Cys Lys Asp Ile Asn Asn Asp Tyr Leu Ala Glu Arg
114                     305                      310                      315                      320
115  Ser Ile Glu Glu Val Tyr Tyr Leu Trp Cys Leu Ala Gly Gly Asp Leu
116                      325                      330                      335
117  Glu Lys Glu Leu Val Asn Lys Glu Ile Ile Arg Ser Lys Pro Pro Ile
118                      340                      345                      350
119  Cys Thr Leu Pro Asn Phe Leu Phe Glu Asp Gly Glu Ser Phe Gly Gln
120                      355                      360                      365
121  Gly Arg Asp Arg Ser Ser Leu Leu Asp Asp Thr Thr Val Thr Leu Ser
122                     370                      375                      380
123  Leu Cys Gln Leu Arg Asn Arg Leu Lys Asp Val Gly Gly Glu Ala Phe
124                     385                      390                      395                      400
125  Tyr Pro Leu Leu Glu Asp Asp Gln Ser Asn Leu Pro His Ser Asn Ser
126                      405                      410                      415
127  Asn Asn Glu Leu Ser Ala Ala Ala Thr Leu Pro Leu Ile Ile Arg Glu
128                      420                      425                      430
129  Lys Asp Thr Glu Tyr Gln Leu Asn Arg Ile Ile Leu Phe Asp Arg Leu
130                      435                      440                      445
131  Leu Lys Ala Tyr Pro Tyr Lys Lys Asn Gln Ile Trp Lys Glu Ala Arg
132                     450                      455                      460
133  Val Asp Ile Pro Pro Leu Met Arg Gly Leu Thr Trp Ala Ala Leu Leu
134                     465                      470                      475                      480
135  Gly Val Glu Gly Ala Ile His Ala Lys Tyr Asp Ala Ile Asp Lys Asp
136                      485                      490                      495
137  Thr Pro Ile Pro Thr Asp Arg Gln Ile Glu Val Asp Ile Pro Arg Cys
138                      500                      505                      510
139  His Gln Tyr Asp Glu Leu Leu Ser Pro Glu Gly His Ala Lys Phe
140                      515                      520                      525
141  Arg Arg Val Leu Lys Ala Trp Val Val Ser His Pro Asp Leu Val Tyr
142                     530                      535                      540
143  Trp Gln Gly Leu Asp Ser Leu Cys Ala Pro Phe Leu Tyr Leu Asn Phe

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144	545	550	555	560
145	Asn Asn Glu Ala Leu Ala Tyr Ala Cys Met Ser Ala Phe Ile Pro Lys			
146		565	570	575
147	Tyr Leu Tyr Asn Phe Phe Leu Lys Asp Asn Ser His Val Ile Gln Glu			
148		580	585	590
149	Tyr Leu Thr Val Phe Ser Gln Met Ile Ala Phe His Asp Pro Glu Leu			
150		595	600	605
151	Ser Asn His Leu Asn Glu Ile Gly Phe Ile Pro Asp Leu Tyr Ala Ile			
152		610	615	620
153	Pro Trp Phe Leu Thr Met Phe Thr His Val Phe Pro Leu His Lys Ile			
154		625	630	635
155	Phe His Leu Trp Asp Thr Leu Leu Leu Gly Asn Ser Ser Phe Pro Phe			
156		645	650	655
157	Cys Ile Gly Val Ala Ile Leu Gln Gln Leu Arg Asp Arg Leu Leu Ala			
158		660	665	670
159	Asn Gly Phe Asn Glu Cys Ile Leu Leu Phe Ser Asp Leu Pro Glu Ile			
160		675	680	685
161	Asp Ile Glu Arg Cys Val Arg Glu Ser Ile Asn Leu Phe Cys Trp Thr			
162		690	695	700
163	Pro Lys Ser Ala Thr Tyr Arg Gln His Ala Gln Pro Pro Lys Pro Ser			
164		705	710	715
165	Ser Asp Ser Ser Gly Gly Arg Ser Ser Ala Pro Tyr Phe Ser Ala Glu			
166		725	730	735
167	Cys Pro Asp Pro Pro Lys Thr Asp Leu Ser Arg Glu Ser Ile Pro Leu			
168		740	745	750
169	Asn Asp Leu Lys Ser Glu Val Ser Pro Arg Ile Ser Ala Glu Asp Leu			
170		755	760	765
171	Ile Asp Leu Cys Glu Leu Thr Val Thr Gly His Phe Lys Thr Pro Ser			
172		770	775	780
173	Lys Lys Thr Lys Ser Ser Lys Pro Lys Leu Leu Val Val Asp Ile Arg			
174		785	790	795
175	Asn Ser Glu Asp Phe Ile Arg Gly His Ile Ser Gly Ser Ile Asn Ile			
176		805	810	815
177	Pro Phe Ser Ala Ala Phe Thr Ala Glu Gly Glu Leu Thr Gln Gly Pro			
178		820	825	830
179	Tyr Thr Ala Met Leu Gln Asn Phe Lys Gly Lys Val Ile Val Ile Val			
180		835	840	845
181	Gly His Val Ala Lys His Thr Ala Glu Phe Ala Ala His Leu Val Lys			
182		850	855	860
183	Met Lys Tyr Pro Arg Ile Cys Ile Leu Asp Gly Gly Ile Asn Lys Ile			
184		865	870	875
185	Lys Pro Thr Gly Leu Leu Thr Ile Pro Ser Pro Gln Ile			
186		885	890	

**VERIFICATION SUMMARY**

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